```
1    ATGGTAAACCGATTGTCAATACCAAAGCCCAACTTAAATTCAACGGGAGTCAACATGATGTCCAATGTTCACCTGCAGCAAAACAACTATGGAGTCAAA
     M  V  N  R  L  S  I  P  K  P  N  L  N  S  T  G  V  N  M  M  S  N  V  H  L  Q  Q  N  N  Y  G  V  K     33
100  TCTGTGGGCCAGAGCTATGGTGTTGGCCAGTCAGTGAGGCTGGGACTAGGTGGCAATGCTCCAGTTTCCATCCCTCAACAGTCTCAGTCCGTGAAACAG
     S  V  G  Q  S  Y  G  V  G  Q  S  V  R  L  G  L  G  G  N  A  P  V  S  I  P  Q  Q  S  Q  S  V  K  Q     66
199  TTACTTCCAAGTGGGAATGGGAGGTCTTTTGGGCTAGGTGCTGAGCAGAGGCCCCCAGCAGCAGCCAGGTACTCCCTGCAGACTGCCAACACCTCTCTA
     L  L  P  S  G  N  G  R  S  F  G  L  G  A  E  Q  R  P  P  A  A  A  R  Y  S  L  Q  T  A  N  T  S  L     99
298  CCCCCAGGCCAAGTGAAGTCTCCCTCTGTGTCTCAGTCACAGGCATCTAGAGTATTAGGTCAGTCCAGTTCTAAACCTCCACCAGCCGCCACAGGCCCT
     P  P  G  Q  V  K  S  P  S  V  S  Q  S  Q  A  S  R  V  L  G  Q  S  S  S  K  P  P  P  A  A  T  G  P     132
397  CCTCCAAGCAACCACTGTGCCACTCAGAAGTGGAAAATCTGTACAATCTGTAACGAGCTTTTCCCTGAGAATGTCTATAGCGTTCACTTCGAAAAGGAG
     P  P  S  N  H  C  A  T  Q  K  W  K  I  C  T  I  C  N  E  L  F  P  E  N  V  Y  S  V  H  F  E  K  E     165
496  CATAAAGCTGAGAAAGTCCCAGCCGTAGCTAACTACATTATGAAAATACACAATTTTACTAGCAAATGCCTCTACTGTAATCGCTATTTGCCTACAGAT
     H  K  A  E  K  V  P  A  V  A  N  Y  I  M  K  I  H  N  F  T  S  K  C  L  Y  C  N  R  Y  L  P  T  D     198
595  ACCCTACTCAACCATATGTTAATTCATGGTCTGTCTTGTCCGTATTGCCGTTCCACCTTCAATGATGTAGAGAAGATGGCAGCACACATGCGAATGGTT
     T  L  L  N  H  M  L  I  H  G  L  S  C  P  Y  C  R  S  T  F  N  D  V  E  K  M  A  A  H  M  R  M  V     231
694  CATATTGATGAAGAGATGGGGCCTAAAACGGATTCTACTTTGAGCTTTGATTTGACATTGCAACAGGGCAGTCACACCAACATTCATCTCCTGGTGACC
     H  I  D  E  E  M  G  P  K  T  D  S  T  L  S  F  D  L  T  L  Q  Q  G  S  H  T  N  I  H  L  L  V  T     264
793  ACATACAACCTGAGGGATGCCCCGGCTGAATCAGTTGCTTACCATGCCCAAAATAATGCCCCAGTTCCTCCAAAGCCACAACCAAAAGTTCAGGAAAAA
     T  Y  N  L  R  D  A  P  A  E  S  V  A  Y  H  A  Q  N  N  A  P  V  P  P  K  P  Q  P  K  V  Q  E  K     297
892  GCAGATGTCCCGGTTAAAAGTTCACCTCAAGCTGCAGTGCCCTATAAAAAAGATGTTGGGAAGACCCTTTGCCCTCTTTGCTTTTCAATACTAAAAGGA
     A  D  V  P  V  K  S  S  P  Q  A  A  V  P  Y  K  K  D  V  G  K  T  L  C  P  L  C  F  S  I  L  K  G     330
991  CCCATATCTGATGCACTTGCACATCATTTACGAGAAAGACACCAAGTTATTCAGACAGTTCATCCGGTTGAGAAAAAGCTAACTTACAAATGTATCCAT
     P  I  S  D  A  L  A  H  H  L  R  E  R  H  Q  V  I  Q  T  V  H  P  V  E  K  K  L  T  Y  K  C  I  H     363
1090 TGCCTTGGTGTGTATACTAGCAACATGACAGCCTCAACCATCACTCTGCATCTAGTCCACTGCAGGGGTGTTGGAAAAACCCAGAATGGCCAGGACAAG
     C  L  G  V  Y  T  S  N  M  T  A  S  T  I  T  L  H  L  V  H  C  R  G  V  G  K  T  Q  N  G  Q  D  K     396
1189 ACAAACGCACCTTCTCGGCTCAATCAGTCTCCAGGCCTGGCCCCTGTGAAGCGCACGTATGAGCAGATGGAGTTTCCACTGCTAAAAAAGCGGAAGCTG
     T  N  A  P  S  R  L  N  Q  S  P  G  L  A  P  V  K  R  T  Y  E  Q  M  E  F  P  L  L  K  K  R  K  L     429
1288 GAGGAGGATGCTGATTCCCCTAGCTGCTTTGAAGAGAAGCCAGAAGAGCCTGTTGTTTTAGCTTTAGACCCCAAGGGTCATGAAGATGATTCTTATGAG
     E  E  D  A  D  S  P  S  C  F  E  E  K  P  E  E  P  V  V  L  A  L  D  P  K  G  H  E  D  D  S  Y  E     462
1387 GCTAGGAAAAGCTTTCTCACAAAGTACTTCAACAAACAGCCCTATCCCACCAGGAGAGAAATTGAGAAGTTAGCTGCCAGTCTATGGCTATGGAAGAGT
     A  R  K  S  F  L  T  K  Y  F  N  K  Q  P  Y  P  T  R  R  E  I  E  K  L  A  A  S  L  W  L  W  K  S     495
1486 GACATTGCCTCCCATTTCAGTAACAAGAGGAAGAAGTGTGTCCGCGACTGTGAAAAGTACAAGCCTGGTGTGCTGCTAGGTTTTAACATGAAAGAATTA
     D  I  A  S  H  F  S  N  K  R  K  K  C  V  R  D  C  E  K  Y  K  P  G  V  L  L  G  F  N  M  K  E  L     528
1585 AATAAAGTCAAACACGAGATGGATTTTGATGCTGAGTGGCTGTTTGAAAATCACGATGAGAAAGACTCAAGAGTCAATGCTAGCAAGACTGTTGACAAA
     N  K  V  K  H  E  M  D  F  D  A  E  W  L  F  E  N  H  D  E  K  D  S  R  V  N  A  S  K  T  V  D  K     561
1684 AAGCATAACCTTGGGAAAGAAGATGATAGCTTCTCAGATAGTTTTGAACATTTGGAAGAAGAATCCAATGGAAGCGGGAGTCCTTTTGACCCTGTCTTT
     K  H  N  L  G  K  E  D  D  S  F  S  D  S  F  E  H  L  E  E  E  S  N  G  S  G  S  P  F  D  P  V  F     594
1783 GAAGTTGAGCCTAAAATTCCCAGTGATAATTTAGAGGAGCCTGTACCGAAGGTTATTCCGGAAGGTGCTTTGGAATCTGAGAAGCTAGACCAAAAAGAG
     E  V  E  P  K  I  P  S  D  N  L  E  E  P  V  P  K  V  I  P  E  G  A  L  E  S  E  K  L  D  Q  K  E     627
```

FIG. 1A.

```
1882 GAGGAGGAGGAGGAGGAGGAGGAGGATGGTTCAAAATATGAAACTATCCATTTGACTGAGGAACCAGCCAAATTAATGCATGATGCCTCTGATAGTGAG
     E  E  E  E  E  E  E  E  D  G  S  K  Y  E  T  I  H  L  T  E  E  P  A  K  L  M  H  D  A  S  D  S  E     660
1981 GTAGACCAAGATGATGTAGTTGAGTGGAAAGATGGTGCTTCACCATCTGAGAGTGGGCCTGGTTCCCAACAAATCTCAGACTTTGAGGATAATACATGT
     V  D  Q  D  D  V  V  E  W  K  D  G  A  S  P  S  E  S  G  P  G  S  Q  Q  I  S  D  F  E  D  N  T  C     693
2080 GAAATGAAACCAGGAACCTGGTCTGATGAGTCTTCCCAGAGTGAAGATGCAAGGAGCAGTAAGCCAGCTGCCAAAAAAAAGGCTACAGTGCAAGATGAC
     E  M  K  P  G  T  W  S  D  E  S  S  Q  S  E  D  A  R  S  S  K  P  A  A  K  K  K  A  T  V  Q  D  D     726
2179 ACAGAGCAGTTAAAATGGAAGAATAGTTCCTATGGAAAAGTTGAAGGGTTTTGGTCCAAGGACCAGTCACAGTGGGAAAATGCATCTGAGAATGCAGAG
     T  E  Q  L  K  W  K  N  S  S  Y  G  K  V  E  G  F  W  S  K  D  Q  S  Q  W  E  N  A  S  E  N  A  E     759
2278 CGCTTACCAAACCCACAGATTGAGTGGCAGAATAGCACAATTGACAGTGAGGACGGGGAGCAGTTTGACAGCATGACTGACGGAGTTGCTGATCCCATG
     R  L  P  N  P  Q  I  E  W  Q  N  S  T  I  D  S  E  D  G  E  Q  F  D  S  M  T  D  G  V  A  D  P  M     792
2377 CATGGCAGCTTAACTGGAGTGAAGCTGAGCAGCCAGCAAGCCTGA
     H  G  S  L  T  G  V  K  L  S  S  Q  Q  A  *                                                             806
```

Single Underline - homologies to HSP60 of ADNP
Dotted Underline - homologies to PIF1 of ADNP
Double Underline - Glycosilation site (amino acid no. 96-98, 183-185, 371-373, 404-406, 554-556, 584-586, 734-736, 753-755, 770-772)
Bold + *Italic* - represents two motifs:

1. Glutaredoxin active site (amino acid no. 211-221)
2. Zinc finger C2h2 type, domain (amino acid no. 211-232)

FIG. 1B.

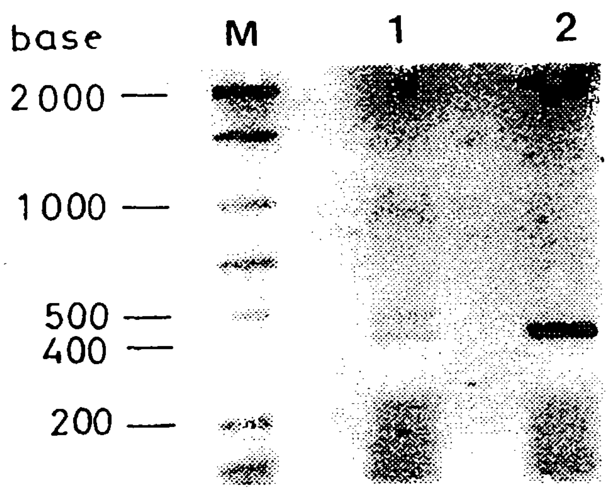


FIG. 2.

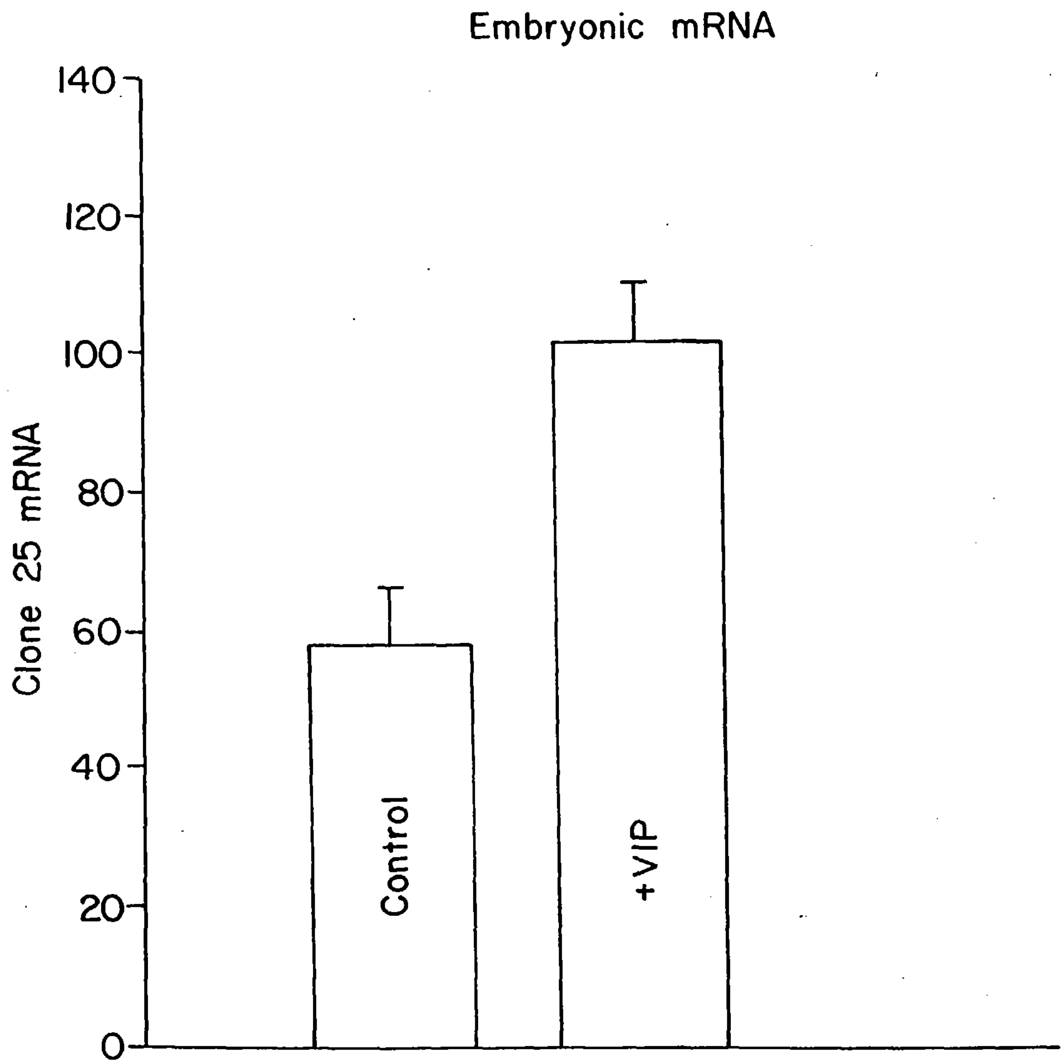

Embryonic mRNA
Clone 25 mRNA
140
120
100
80
60
40
20
0
Control
+VIP

FIG. 3

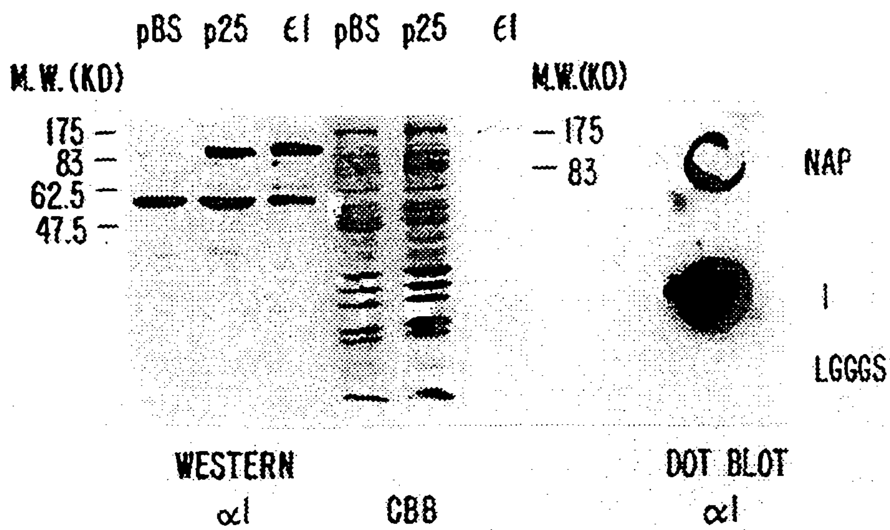

pBS
p25
€I
pBS
p25
€I
M.W.(KD)
175
83
62.5
47.5
M.W.(KD)
175
83
NAP
I
LGGGS
WESTERN
αI
CBB
DOT BLOT
αI

FIG. 4A.

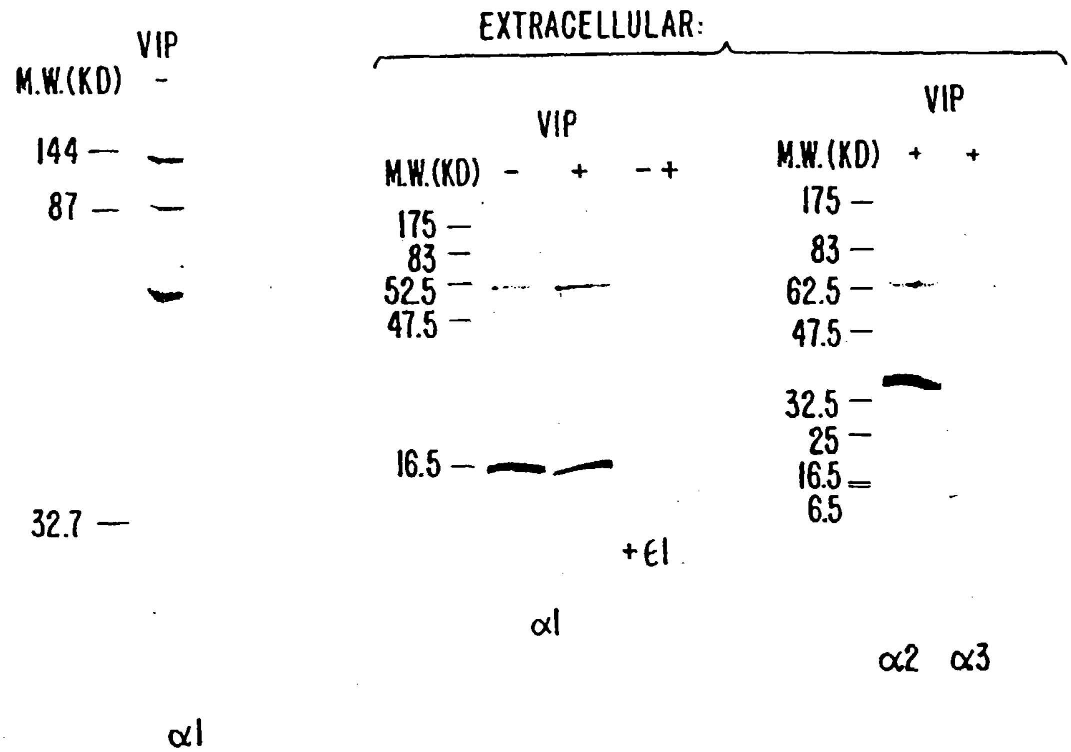
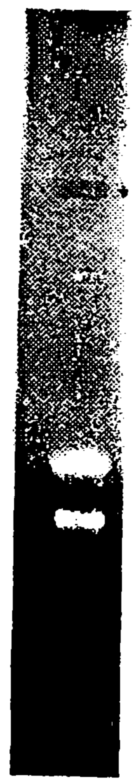

VIP
M.W.(KD) -
144 —
87 —
32.7 —
αl
EXTRACELLULAR:
VIP
M.W.(KD) - + - +
175 —
83 —
52.5 —
47.5 —
16.5 —
+El
αl
VIP
M.W.(KD) + +
175 —
83 —
62.5 —
47.5 —
32.5 —
25 —
16.5 —
6.5
α2 α3

FIG. 4B.

390bp –



Neuroblastoma (NMB)

FIG. 5A.

SENSE

1 CATTGGGCCG ACGTCGCATG CTCCCGGCCG CCATGGCCGC GGGATTACCT
51 GCAGCAAAAC AACTATGGAG TCAAATCTGT AGGCCAGGGT TACAGTGTTG
101 GTCAGTCAAT GAGACTGGGT CTAGGTGGCA ACGCACCAGT TTCCATTCCT
151 CAACAATCTC AGTCTGTAAA GCAGTTACTT CCAAGTGGAA ACGGAAGGTC
201 TTATGGGCTT GGGTCAGAGC AGAGGTCCCA GGCACCAGCA AGATACTCCC
251 TGCAGTCTGC TAATGCCTCT TCTCTCTCAT CGGGCCAGTT AAAGTCTCCT
301 TCCCTCTCTC AGTCACAGGC ATCCAGAGTG TTAGGTCAGT CCAGTTCCAA
351 ACCTGCTGCA GCTGCCACAG GCCCTCCCCC AGGTAACACT TCCTCAACTC
401 AAAAGTGGAA AATATGTACA ATCTGTAACG AGCAATCACT AGTGCGGCCG
451 CCTGCAGGTC GACCATATGG GAGAGCTCCC AACGCGTTGG ATGCATAGCT
501 TGAGTATTCT ATAGTGTCAC CTAAATAGCT TGGCGTAATC ATGGTCATAG
551 CTGTTTCCTG TGTGAAATTG TTATCCGCTC ACAATTCCAC ACAACATACG
601 AACCGGAAGC ATAAAGTGTA AAGCCTGGGG TGCCTAATGA ATGAGCTAAC
651 TCACATTAAT TGCGTTGCGC TCACTGCCCG CTTTCCAATC NGGAAACTGT
701 CGTGCCAACT GCATTAATGA ATCGGCCAAC GCGCGGGGAA AAGCGGTTTG
751 CGTATTGGGC GCTCTTCCGC TTCCTCGCTC AATGAATCCC TGCGCTCNGT
801 CCTTCCGNTG CGGNNAACGG TATCACTCAC TCNAATT

ANTISENSE

1 ATNNATATCA AGCTATGCAT CCAACGCGTT GGGAGCTCTC CCATATGGTC
51 GACCTGCAGG CGGCCGCACT AGTGATTGCT CGTTACAGAT TGTACATATT PRIMER 44
101 TTCCACTTTT GAGTTGAGGA AGTGTTACCT GGGGGAGGGC CTGTGGCAGC
151 TGCAGCAGGT TTGGAACTGG ACTGACCTAA CACTCTGGAT GCCTGTGACT
201 GAGAGAGGGA AGGAGACTTT AACTGGCCCG ATGAGAGAGA AGAGGCATTA
251 GCAGACTGCA GGGAGTATCT TGCTGGTGCC TGGGACCTCT GCTCTGACCC
301 AAGCCCATAA GACCTTCCGT TTCCACTTGG AAGTAACTGC TTTACAGACT
351 GAGATTGTTG AGGAATGGAA ACTGGTGCGT TGCCACCTAG ACCCAGTCTC
401 ATTGACTGAC CAACACTGTA ACCCTGGCCT ACAGATTTGA CTCCATAGTT –PRIMER 105
451 GTTTTGCTGC AGGTAATCCC GCGGCCATGG CGGCCGGGAG CATGCGACGT

FIG. 5B-1.

501 CGGGCCCAAT TCGCCCTATA GTGAGTCGTA TTACAATTCA CTGGCCGTCG

551 TTTTACAACG TCGTGACTGG GAAAACCCTG GCGTTACCCA ACTTAATCCC

601 CTTGCAGCAC ATCCCCCTTT CGCCAGCTGG CGTTAATAAC GAAGAAGCCC

651 GCACCGATCG CCCTTCCCAA CAGTTGCGCA GCCTGAATGG CGAATGGACG

701 CGCCTGTTAG CGCGCATTAA ACCCCGCGGG TGTTGTGGTT ACGCCGCAGC

751 GTGACCGCTA CACTTGCCAC CCCCTAACGC CCGCTCCTTT CCCTTTCTTC

801 CTTCCTTTCT CGCCACGTCC CCCGNTTTCC CCGTCCAACT CTAAATCGGT

FIG. 5B-2.

```
1    MSNVHLQQNNYGVKSVGQSYGVGQSVRLGLGGNAPVSIPQQSQSVKQLLP   50
     ||.||||||||||||||| | ||||.||||||||||||||||||||||||
20   MSSVHLQQNNYGVKSVGQGYSVGQSMRLGLGGNAPVSIPQQSQSVKQLLP   69

51   SGNGRSFGLGAEQRPPAAARYSLQTAN.TSLPPGQVKSPSVSQSQASRVL   99
     ||||||:|||.|||  | ||||||.|| .||  | .||||.| |||||||
70   SGNGRSYGLGSEQRSQAPARYSLQSANASSLSSGHLKSPSLSHSQASRVL   119

100  GQSSSKPPPAATGPPPSNHCATQKWKICTICNELFPENVYSVHFEKEHKA   149
     |||||||  |||||||  |  .|||||||||||||||||||||||||||
120  GQSSSKPAAAATGPPPGNTSSTQKWKICTICNELFPENVYSVHFEKEHKA   169

150  EKVPAVANYIMKIHNFTSKCLYCNRYLPTDTLLNHMLIHGLSCPYCRSTF   199
     ||||||||||||||||||||||||||||||||||||||||||||||||||
170  EKVPAVANYIMKIHNFTSKCLYCNRYLPTDTLLNHMLIHGLSCPYCRSTF   219

200  NDVEKMAAHMRMVHIDEEMGPKTDSTLSFDLTLQQGSHTNIHLLVTTYNL   249
     ||||||||||||||||||||||||||||||||||||||||||||||||||
220  NDVEKMAAHMRMVHIDEEMGPKTDSTLSFDLTLQQGSHTNIHLLVTTYNL   269

250  RDAPAESVAYHAQNNAPVPPKPQPKVQEKADVPVKSSPQAAVPYKKDVGK   299
     ||||||||||||||| |||||||||||||||:||||||||||||||||||
270  RDAPAESVAYHAQNNPPVPPKPQPKVQEKADIPVKSSPQAAVPYKKDVGK   319

300  TLCPLCFSILKGPISDALAHHLRERHQVIQTVHPVEKKLTYKCIHCLGVY   349
     ||||||||||||||||||||||||||||||||||||||||||||||||||
320  TLCPLCFSILKGPISDALAHHLRERHQVIQTVHPVEKKLTYKCIHCLGVY   369

350  TSNMTASTITLHLVHCRGVGKTQNGQDKTNAPSRLNQSPGLAPVKRTYEQ   399
     ||||||||||||||||||||||||||||||||||||||| ||||||||||
370  TSNMTASTITLHLVHCRGVGKTQNGQDKTNAPSRLNQSPSLAPVKRTYEQ   419

400  MEFPLLKKRKLEEDADSPSCFEEKPEEPVVLALDPKGHEDDSYEARKSFL   449
     |||||||||||::|.|||| ||||||||||||||||||||||||||||||
420  MEFPLLKKRKLDDDSDSPSFFEEKPEEPVVLALDPKGHEDDSYEARKSFL   469

450  TKYFNKQPYPTRREIEKLAASLWLWKSDIASHFSNKRKKCVRDCEKYKPG   499
     ||||||||||||||||||||||||||||||||||||||||||||||||||
470  TKYFNKQPYPTRREIEKLAASLWLWKSDIASHFSNKRKKCVRDCEKYKPG   519

500  VLLGFNMKELNKVKHEMDFDAEWLFENHDEKDSRVNASKTVDKKHNLGKE   549
     |||||||||||||||||||||||||||||||||||||||| ||| |||||
520  VLLGFNMKELNKVKHEMDFDAEWLFENHDEKDSRVNASKTADKKLNLGKE   569

550  DDSFSDSFEHLEEESNGSGSPFDPVFEVEPKIPSDNLEEPVPKVIPEGAL   599
     ||| |||||.|||||| ||||||||||||||| .|| || | ||||| |
570  DDSSSDSFENLEEESNESGSPFDPVFEVEPKISNDNPEEHVLKVIPEDAS   619

600  ESEKLDQKEEEEEEEEEDGSKYETIHLTEEPAKLMHDASDSEVDQDDVVE   649
     ||       ||. ::.||||||||||||||| ||||.|||||||||||||
620  ES.......EEKLDQKEDGSKYETIHLTEEPTKLMHNASDSEVDQDDVVE   662

650  WKDGASPSESGPGSQQISDFEDNTCEMKPGTWSDESSQSEDARSSKPAAK   699
     ||||||||||||||||:|||||||||||||||||||||||||||||||||
663  WKDGASPSESGPGSQQVSDFEDNTCEMKPGTWSDESSQSEDARSSKPAAK   712

700  KKATVQDDTEQLKWKNSSYGKVEGFWSKDQSQWENASENAERLPNPQIEW   749
     ||||.| | ||||||||||||||||||||||||.||||| ||| ||||||
713  KKATMQGDREQLKWKNSSYGKVEGFWSKDQSQWKNASENDERLSNPQIEW   762
```

FIG. 5C-1.

```
750 QNSTIDSEDGEQFDSMTDGVADPMHGSLTGVKLSSQQA  787
    ||||||||||||||.||||| :|||||| |||||||||
763 QNSTIDSEDGEQFDNMTDGVTEPMHGSLAGVKLSSQQA  800
```

FIG. 5C-2.

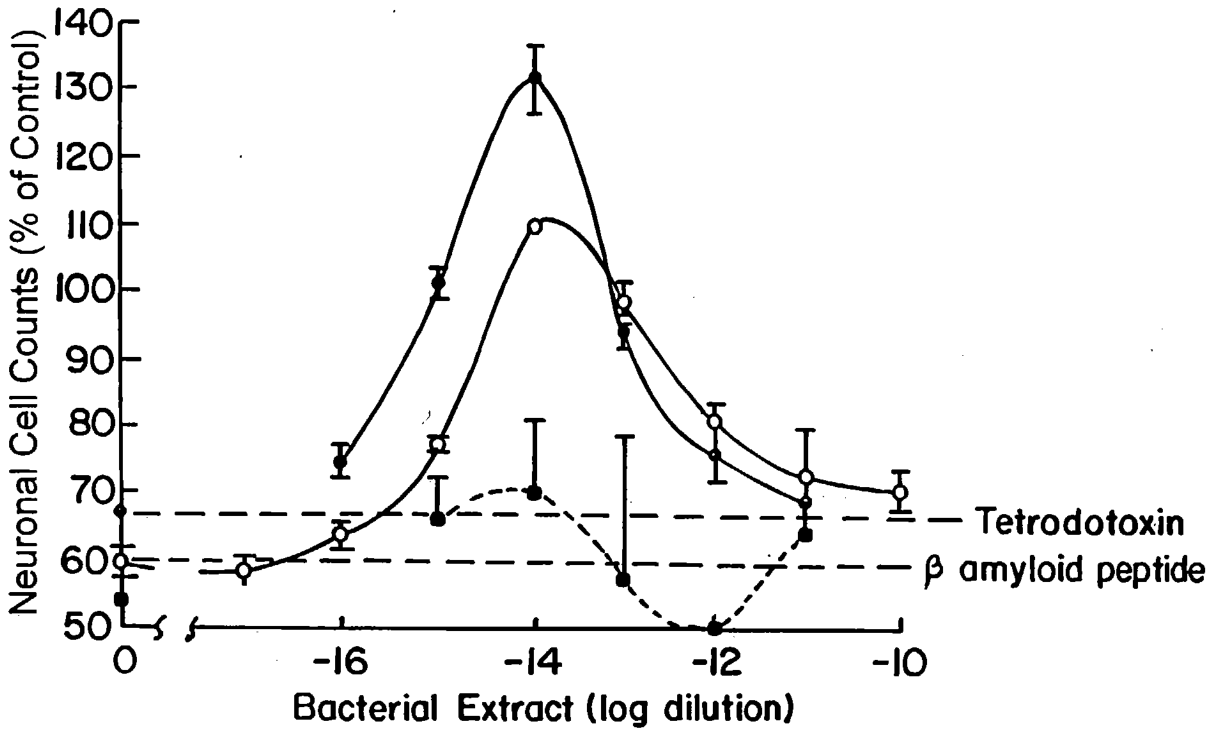

Neuronal Cell Counts (% of Control)
140
130
120
110
100
90
80
70
60
50
0
-16
-14
-12
-10
Bacterial Extract (log dilution)
Tetrodotoxin
β amyloid peptide

FIG. 6A

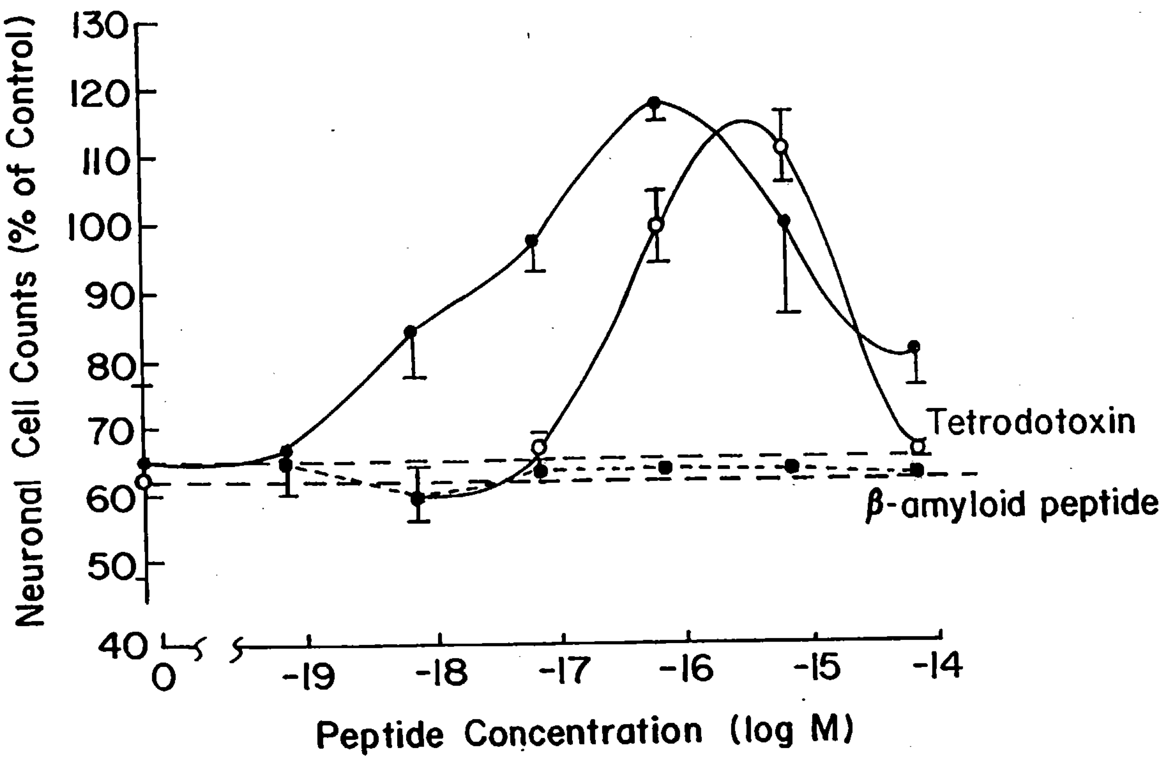

Neuronal Cell Counts (% of Control)
130
120
110
100
90
80
70
60
50
40
0
-19
-18
-17
-16
-15
-14
Peptide Concentration (log M)
Tetrodotoxin
β-amyloid peptide

FIG. 6B

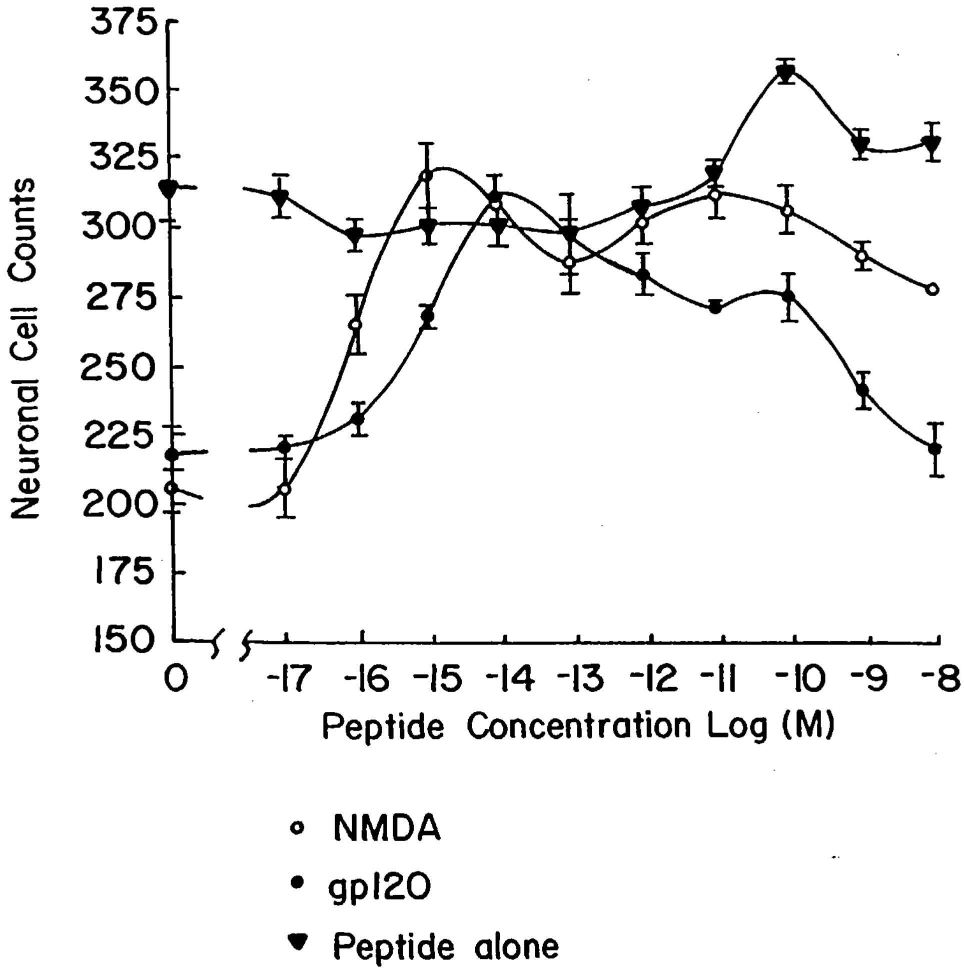

375
350
325
300
275
250
225
200
175
150
Neuronal Cell Counts
0
-17
-16
-15
-14
-13
-12
-11
-10
-9
-8
Peptide Concentration Log (M)
NMDA
gp120
Peptide alone

FIG. 6C

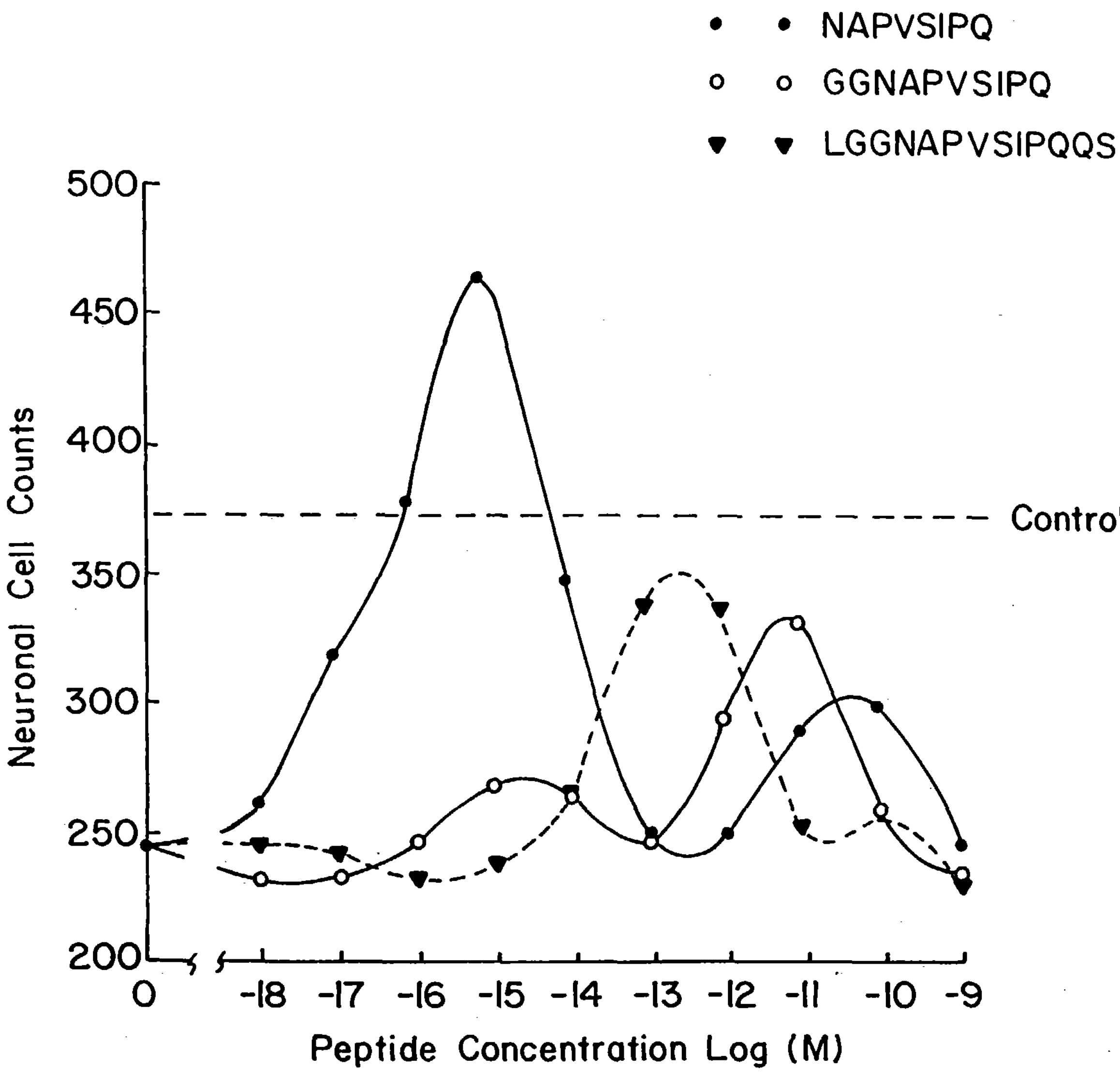

NAPVSIPQ
GGNAPVSIPQ
LGGNAPVSIPQQS
500
450
400
350
300
250
200
Neuronal Cell Counts
Control
0
-18
-17
-16
-15
-14
-13
-12
-11
-10
-9
Peptide Concentration Log (M)

FIG. 7A

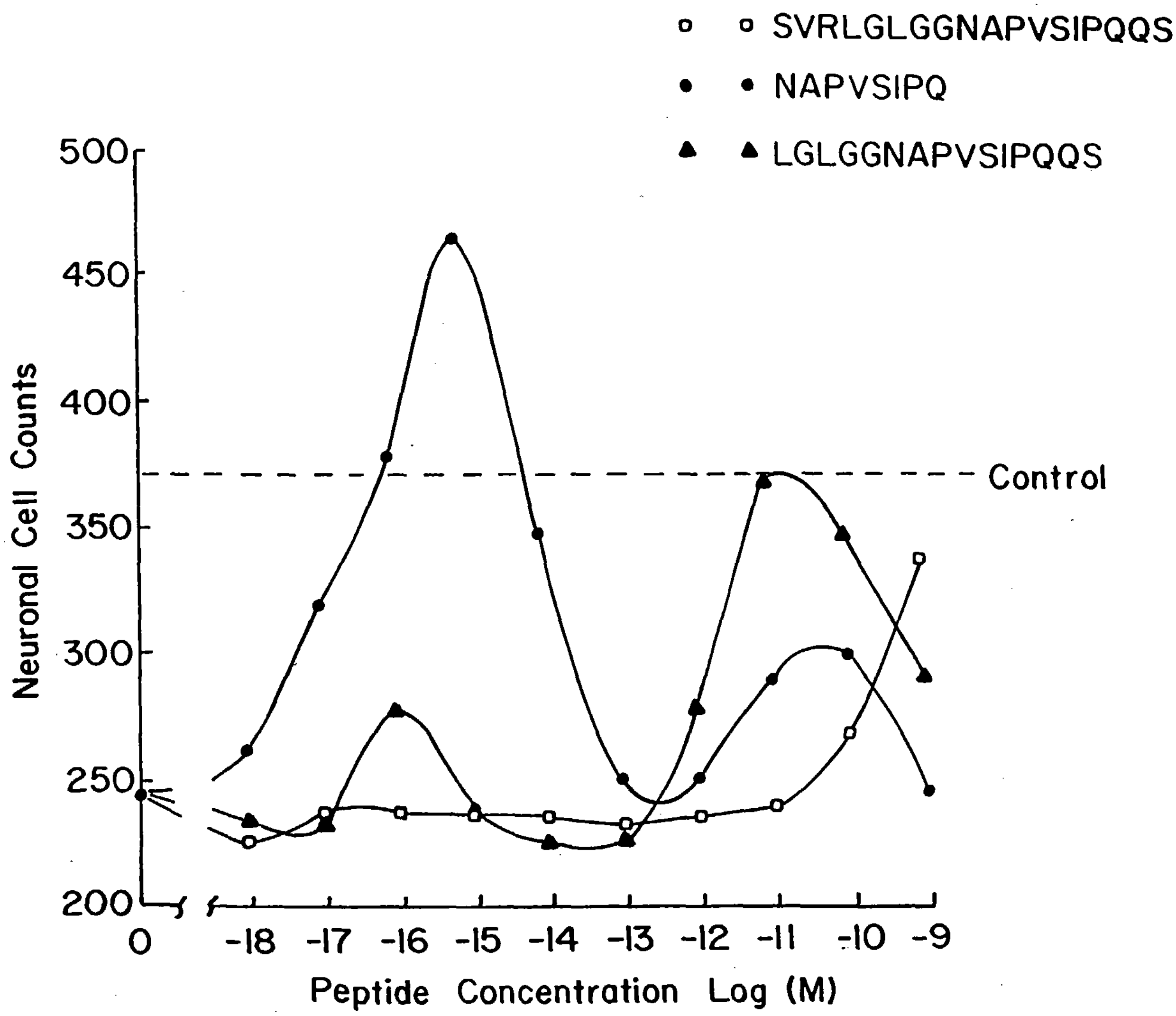

SVRLGLGGNAPVSIPQQS
NAPVSIPQ
LGLGGNAPVSIPQQS
500
450
400
350
300
250
200
Neuronal Cell Counts
Control
0
-18
-17
-16
-15
-14
-13
-12
-11
-10
-9
Peptide Concentration Log (M)

FIG. 7B

The effect of NAPVSIPQ(NAP) on learning and memory

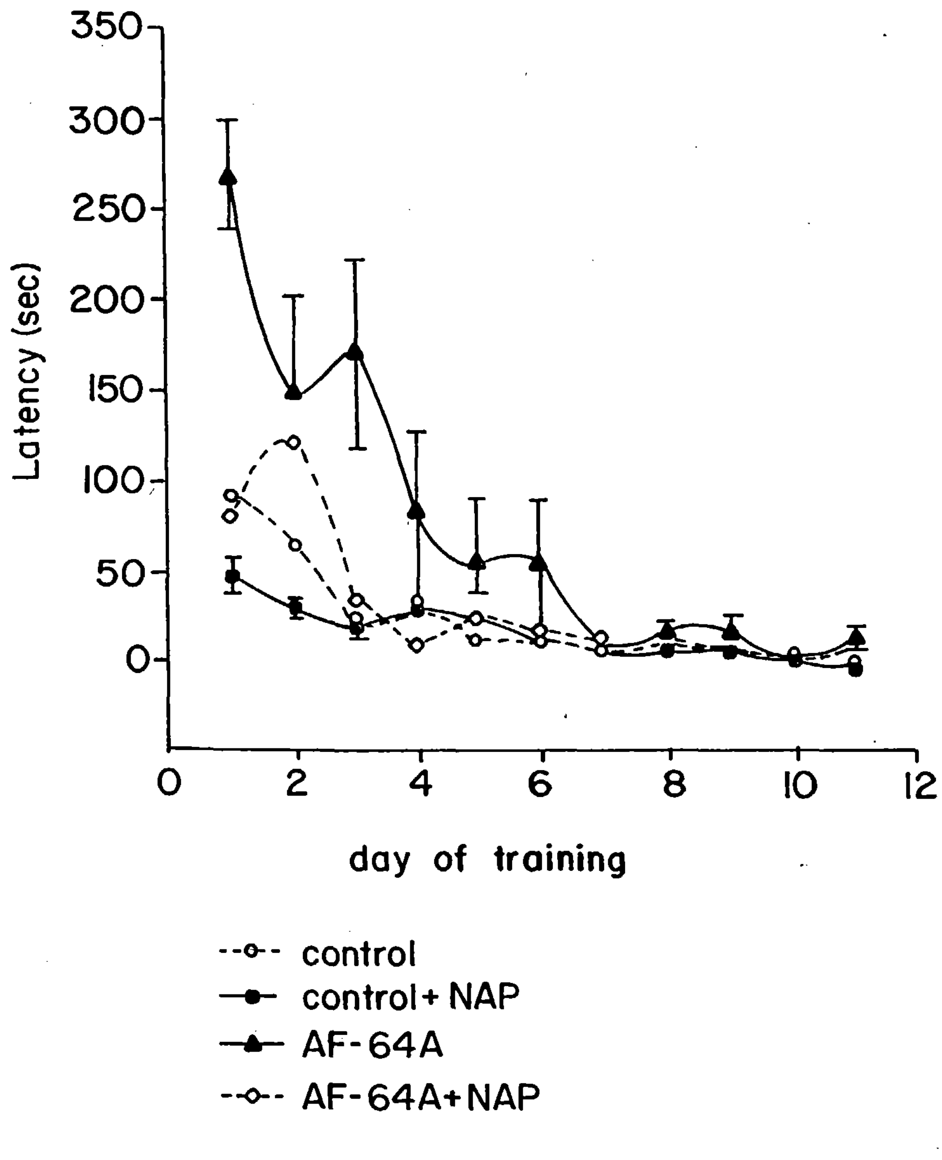


FIG. 8

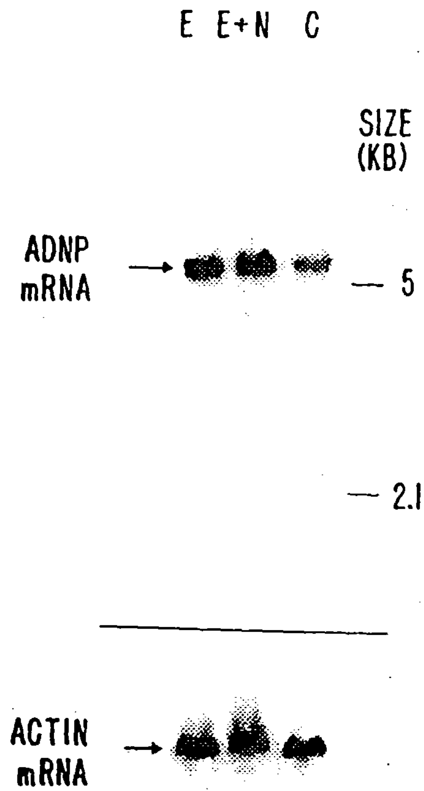


FIG. 9.

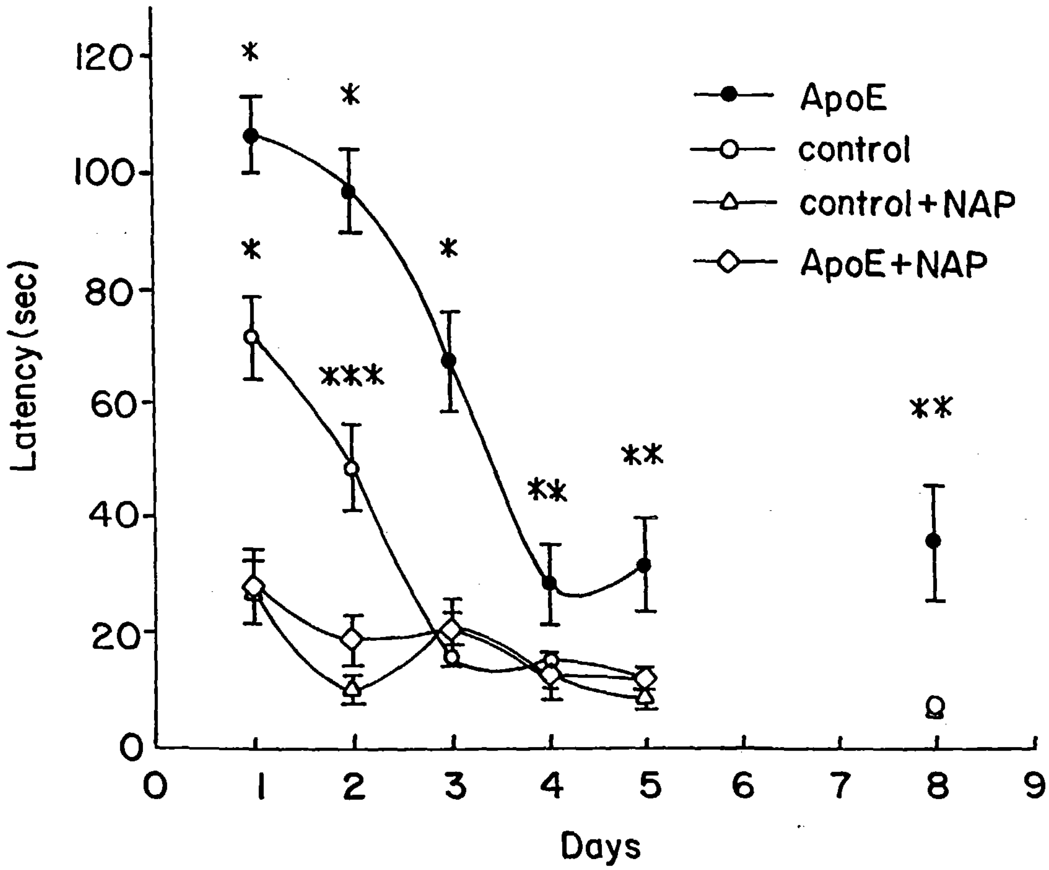

120
100
80
60
40
20
0
Latency (sec)
0
1
2
3
4
5
6
7
8
9
Days
ApoE
control
control+NAP
ApoE+NAP
*
*
*
*
***
**
**
**

FIG. 10

20/31

```
1     ATGGGACTCCCACCACGAATCAGCTCCCTTGCTTCTGGAAATGTCCGGTCGTTGCCATCACAGCAGATGGTAAACCGATTGTCAATACCAAAGCCCAAC
      M  G  L  P  P  R  I  S  S  L  A  S  G  N  V  R  S  L  P  S  Q  Q  M  V  N  R  L  S  I  P  K  P  N     33
100   TTAAATTCAACGGGAGTCAACATGATGTCCAATGTTCACCTGCAGCAAAACAACTATGGAGTCAAATCTGTGGGCCAGAGCTATGGTGTTGGCCAGTCA
      L  N  S  T  G  V  N  M  M  S  N  V  H  L  Q  Q  N  N  Y  G  V  K  S  V  G  Q  S  Y  G  V  G  Q  S     66
199   GTGAGGCTGGGACTAGGTGGCAATGCTCCAGTTTCCATCCCTCAACAGTCTCAGTCCGTGAAACAGTTACTTCCAAGTGGGAATGGGAGGTCTTTTGGG
      V  R  L  G  L  G  G  N  A  P  V  S  I  P  Q  Q  S  Q  S  V  K  Q  L  L  P  S  G  N  G  R  S  F  G     99
298   CTAGGTGCTGAGCAGAGGCCCCCAGCAGCAGCCAGGTACTCCCTGCAGACTGCCAACACCTCTCTACCCCCAGGCCAAGTGAAGTCTCCCTCTGTGTCT
      L  G  A  E  Q  R  P  P  A  A  A  R  Y  S  L  Q  T  A  N  T  S  L  P  P  G  Q  V  K  S  P  S  V  S    132
397   CAGTCACAGGCATCTAGAGTATTAGGTCAGTCCAGTTCTAAACCTCCACCAGCCGCCACAGGCCCTCCTCCAAGCAACCACTGTGCCACTCAGAAGTGG
      Q  S  Q  A  S  R  V  L  G  Q  S  S  S  K  P  P  P  A  A  T  G  P  P  P  S  N  H  C  A  T  Q  K  W    165
496   AAAATCTGTACAATCTGTAACGAGCTTTTCCCTGAGAATGTCTATAGCGTTCACTTCGAAAAGGAGCATAAAGCTGAGAAAGTCCCAGCCGTAGCTAAC
      K  I  C  T  I  C  N  E  L  F  P  E  N  V  Y  S  V  H  F  E  K  E  H  K  A  E  K  V  P  A  V  A  N    198
595   TACATTATGAAAATACACAATTTTACTAGCAAATGCCTCTACTGTAATCGCTATTTGCCTACAGATACCCTACTCAACCATATGTTAATTCATGGTCTG
      Y  I  M  K  I  H  N  F  T  S  K  C  L  Y  C  N  R  Y  L  P  T  D  T  L  L  N  H  M  L  I  H  G  L    231
694   TCTTGTCCGTATTGCCGTTCCACCTTCAATGATGTAGAGAAGATGGCAGCACACATGCGAATGGTTCATATTGATGAAGAGATGGGGCCTAAAACGGAT
      S  C  P  Y  C  R  S  T  F  N  D  V  E  K  M  A  A  H  M  R  M  V  H  I  D  E  E  M  G  P  K  T  D    264
793   TCTACTTTGAGCTTTGATTTGACATTGCAACAGGGCAGTCACACCAACATTCATCTCCTGGTGACCACATACAACCTGAGGGATGCCCCGGCTGAATCA
      S  T  L  S  F  D  L  T  L  Q  Q  G  S  H  T  N  I  H  L  L  V  T  T  Y  N  L  R  D  A  P  A  E  S    297
892   GTTGCTTACCATGCCCAAAATAATGCCCCAGTTCCTCCAAAGCCACAACCAAAAGTTCAGGAAAAAGCAGATGTCCCGGTTAAAAGTTCACCTCAAGCT
      V  A  Y  H  A  Q  N  N  A  P  V  P  P  K  P  Q  P  K  V  Q  E  K  A  D  V  P  V  K  S  S  P  Q  A    330
991   GCAGTGCCCTATAAAAAAGATGTTGGGAAGACCCTTTGCCCTCTTTGCTTTTCAATACTAAAAGGACCCATATCTGATGCACTTGCACATCATTTACGA
      A  V  P  Y  K  K  D  V  G  K  T  L  C  P  L  C  F  S  I  L  K  G  P  I  S  D  A  L  A  H  H  L  R    363
1090  GAAAGACACCAAGTTATTCAGACAGTTCATCCGGTTGAGAAAAAGCTAACTTACAAATGTATCCATTGCCTTGGTGTGTATACTAGCAACATGACAGCC
      E  R  H  Q  V  I  Q  T  V  H  P  V  E  K  K  L  T  Y  K  C  I  H  C  L  G  V  Y  T  S  N  M  T  A    396
1189  TCAACCATCACTCTGCATCTAGTCCACTGCAGGGGTGTTGGAAAAACCCAGAATGGCCAGGACAAGACAAACGCACCTTCTCGGCTCAATCAGTCTCCA
      S  T  I  T  L  H  L  V  H  C  R  G  V  G  K  T  Q  N  G  Q  D  K  T  N  A  P  S  R  L  N  Q  S  P    429
1288  GGCCTGGCCCCTGTGAAGCGCACGTATGAGCAGATGGAGTTTCCACTGCTAAAAAAGCGGAAGCTGGAGGAGGATGCTGATTCCCCTAGCTGCTTTGAA
      G  L  A  P  V  K  R  T  Y  E  Q  M  E  F  P  L  L  K  K  R  K  L  E  E  D  A  D  S  P  S  C  F  E    462
1387  GAGAAGCCAGAAGAGCCTGTTGTTTTAGCTTTAGACCCCAAGGGTCATGAAGATGATTCTTATGAGGCTAGGAAAAGCTTTCTCACAAAGTACTTCAAC
      E  K  P  E  E  P  V  V  L  A  L  D  P  K  G  H  E  D  D  S  Y  E  A  R  K  S  F  L  T  K  Y  F  N    495
1486  AAACAGCCCTATCCCACCAGGAGAGAAATTGAGAAGTTAGCTGCCAGTCTATGGCTATGGAAGAGTGACATTGCCTCCCATTTCAGTAACAAGAGGAAG
      K  Q  P  Y  P  T  R  R  E  I  E  K  L  A  A  S  L  W  L  W  K  S  D  I  A  S  H  F  S  N  K  R  K    528
1585  AAGTGTGTCCGCGACTGTGAAAAGTACAAGCCTGGTGTGCTGCTAGGTTTTAACATGAAAGAATTAAATAAAGTCAAACACGAGATGGATTTTGATGCT
      K  C  V  R  D  C  E  K  Y  K  P  G  V  L  L  G  F  N  M  K  E  L  N  K  V  K  H  E  M  D  F  D  A    561
1684  GAGTGGCTGTTTGAAAATCACGATGAGAAAGACTCAAGAGTCAATGCTAGCAAGACTGTTGACAAAAAGCATAACCTTGGGAAAGAAGATGATAGCTTC
      E  W  L  F  E  N  H  D  E  K  D  S  R  V  N  A  S  K  T  V  D  K  K  H  N  L  G  K  E  D  D  S  F    594
1783  TCAGATAGTTTTGAACATTTGGAAGAAGAATCCAATGGAAGCGGGAGTCCTTTTGACCCTGTCTTTGAAGTTGAGCCTAAAATTCCCAGTGATAATTTA
      S  D  S  F  E  H  L  E  E  E  S  N  G  S  G  S  P  F  D  P  V  F  E  V  E  P  K  I  P  S  D  N  L    627
1882  GAGGAGCCTGTACCGAAGGTTATTCCGGAAGGTGCTTTGGAATCTGAGAAGCTAGACCAAAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGATGGTTCA
```

FIG. 11A.

```
     E  E  P  V  P  K  V  I  P  E  G  A  L  E  S  E  K  L  D  Q  K  E  E  E  E  E  E  E  E  D  G  S     660
1981 AAATATGAAACTATCCATTTGACTGAGGAACCAGCCAAATTAATGCATGATGCCTCTGATAGTGAGGTAGACCAAGATGATGTAGTTGAGTGGAAAGAT
     K  Y  E  T  I  H  L  T  E  E  P  A  K  L  M  H  D  A  S  D  S  E  V  D  Q  D  D  V  V  E  W  K  D  693
2080 GGTGCTTCACCATCTGAGAGTGGGCCTGGTTCCCAACAAATCTCAGACTTTGAGGATAATACATGTGAAATGAAACCAGGAACCTGGTCTGATGAGTCT
     G  A  S  P  S  E  S  G  P  G  S  Q  Q  I  S  D  F  E  D  N  T  C  E  M  K  P  G  T  W  S  D  E  S  726
2179 TCCCAGAGTGAAGATGCAAGGAGCAGTAAGCCAGCTGCCAAAAAAAAGGCTACAGTGCAAGATGACACAGAGCAGTTAAAATGGAAGAATAGTTCCTAT
     S  Q  S  E  D  A  R  S  S  K  P  A  A  K  K  K  A  T  V  Q  D  D  T  E  Q  L  K  W  K  N  S  S  Y  759
2278 GGAAAAGTTGAAGGGTTTTGGTCCAAGGACCAGTCACAGTGGGAAAATGCATCTGAGAATGCAGAGCGCTTACCAAACCCACAGATTGAGTGGCAGAAT
     G  K  V  E  G  F  W  S  K  D  Q  S  Q  W  E  N  A  S  E  N  A  E  R  L  P  N  P  Q  I  E  W  Q  N  792
2377 AGCACAATTGACAGTGAGGACGGGGAGCACTTTGACAGCATGACTGACGGAGTTGCTGATCCCATGCATGGCAGCTTAACTGGAGTGAAGCTGAGCAGC
     S  T  I  D  S  E  D  G  E  Q  F  D  S  M  T  D  G  V  A  D  P  M  H  G  S  L  T  G  V  K  L  S  S  825
2476 CAGCAAGCCTGA
     Q  Q  A  *                                                                                          828
```

Single Underline - homologies to HSP60 of ADNP
Double Underline - Glycosilation site (amino acid no. 118-120, 205-207, 393-395, 426-428, 576-578, 606-608, 756-758, 775-777, 792-794)
Bold + *Italic* - represents two motifs:
1. Glutaredoxin active site (amino acid no. 233-243)
2. Zinc finger C2h2 type, domain (amino acid no. 233-254)

Bold - potential proteolytic cleavage sites.

Bold + Underline - putative signal peptide

FIG. 11B.

```
46   CGGTCTTTACCATCACAGCAGATGGTGAATCGACTCTCAATACCAAAGCCTAACTTAAATTCTACAGGAGTCAACATGATGTCCAGTGTTCATCTGCAG
     R  S  L  P  S  Q  Q  M  V  N  R  L  S  I  P  K  P  N  L  N  S  T  G  V  N  M  M  S  S  V  H  L  Q    48
145  CAGAACAACTATGGAGTCAAATCTGTAGGCCAGGGTTACAGTGTTGGTCAGTCAATGAGACTGGGTCTAGGTGGCAACGCACCAGTTTCCATTCCTCAA
     Q  N  N  Y  G  V  K  S  V  G  Q  G  Y  S  V  G  Q  S  M  R  L  G  L  G  G  N  A  P  V  S  I  P  Q    81
244  CAATCTCAGTCTGTAAAGCAGTTACTTCCAAGTGGAAACGGAAGGTCTTATGGGCTTGGGTCAGAGCAGAGGTCCCAGGCACCAGCAAGATACTCCCTG
     Q  S  Q  S  V  K  Q  L  L  P  S  G  N  G  R  S  Y  G  L  G  S  E  Q  R  S  Q  A  P  A  R  Y  S  L    114
343  CAGTCTGCTAATGCCTCTTCTCTCTCATCGGGCCAGTTAAAGTCTCCTTCCCTCTCTCAGTCACAGGCATCCAGAGTGTTAGGTCAGTCCAGTTCCAAA
     Q  S  A  N  A  S  S  L  S  S  G  Q  L  K  S  P  S  L  S  Q  S  Q  A  S  R  V  L  G  Q  S  S  S  K    147
442  CCTGCTGCAGCTGCCACAGGCCCTCCCCCAGGTAACACTTCCTCAACTCAAAAGTGGAAAATATGTACAATCTGTAATGAGCTTTTTCCTGAAAATGTC
     P  A  A  A  A  T  G  P  P  P  G  N  T  S  S  T  Q  K  W  K  I  C  T  I  C  N  E  L  F  P  E  N  V    180
541  TATAGTGTGCACTTCGAAAAAGAACATAAAGCTGAGAAAGTCCCAGCAGTAGCCAACTACATTATGAAAATACACAATTTTACTAGCAAATGCCTCTAC
     Y  S  V  H  F  E  K  E  H  K  A  E  K  V  P  A  V  A  N  Y  I  M  K  I  H  N  F  T  S  K  C  L  Y    213
640  TGTAATCGCTATTTACCCACAGATACTCTGCTCAACCATATGTTAATTCATGGTCTGTCTTGTCCATATTGCCGTTCAACTTTCAATGATGTGGAAAAG
     C  N  R  Y  L  P  T  D  T  L  L  N  H  M  L  I  H  G  L  S  C  P  Y  C  R  S  T  F  N  D  V  E  K    246
739  ATGGCCGCACACATGCGGATGGTTCACATTGATGAAGAGATGGGACCTAAAACAGATTCTACTTTGAGTTTTGATTTGACATTGCAGCAGGGTAGTCAC
     M  A  A  H  M  R  M  V  H  I  D  E  E  M  G  P  K  T  D  S  T  L  S  F  D  L  T  L  Q  Q  G  S  H    279
838  ACTAACATCCATCTCCTGGTAACTACATACAATCTGAGGGATGCCCCAGCTGAATCTGTTGCTTACCATGCCCAAAATAATCCTCCAGTTCCTCCAAAG
     T  N  I  H  L  L  V  T  T  Y  N  L  R  D  A  P  A  E  S  V  A  Y  H  A  Q  N  N  P  P  V  P  P  K    312
937  CCACAGCCAAAGGTTCAGGAAAAGGCAGATATCCCTGTAAAAAGTTCACCTCAAGCTGCAGTGCCCTATAAAAAAGATGTTGGAAAAACCCTTTGTCCT
     P  Q  P  K  V  Q  E  K  A  D  I  P  V  K  S  S  P  Q  A  A  V  P  Y  K  K  D  V  G  K  T  L  C  P    345
1036 CTTTGCTTTTCAATCCTAAAAGGACCCATATCTGATGCACTTGCACATCACTTACGAGAGAGGCACCAAGTTATTCAGACGGTTCATCCAGTTGAGAAA
     L  C  Y  S  I  L  K  G  P  I  S  D  A  L  A  H  H  L  R  E  R  H  Q  V  I  Q  T  V  H  P  V  E  K    378
1135 AAGCTCACCTACAAATGTATCCATTGCCTTGGTGTGTATACCAGCAACATGACCGCCTCAACTATCACTCTGCATCTAGTTCACTGCAGGGGCGTTGGA
     K  L  T  Y  K  C  I  H  C  L  G  V  Y  T  S  N  M  T  A  S  T  I  T  L  H  L  V  H  C  R  G  V  G    411
1234 AAGACCCAAAATGGCCAGGATAAGACAAATGCACCCTCTCGGCTTAATCAGTCTCCAAGTCTGGCACCTGTGAAGCGCACTTACGAGCAAATGGAATTT
     K  T  Q  N  G  Q  D  K  T  N  A  P  S  R  L  N  Q  S  P  S  L  A  P  V  K  R  T  Y  E  Q  M  E  F    444
1333 CCCTTACTGAAAAAACGAAAGTTAGATGATGATAGTGATTCACCCAGCTTCTTTGAAGAGAAGCCTGAAGAGCCTGTTGTTTTAGCTTTAGACCCCAAG
     P  L  L  K  K  R  K  L  D  D  D  S  D  S  P  S  F  F  E  E  K  P  E  E  P  V  V  L  A  L  D  P  K    477
1432 GGTCATGAAGATGATTCCTATGAAGCCAGGAAAAGCTTTCTAACAAAGTATTTCAACAAACAGCCCTATCCCACCAGGAGAGAAATTGAGAAGCTAGCA
     G  H  E  D  D  S  Y  E  A  R  K  S  F  L  T  K  Y  F  N  K  Q  P  Y  P  T  R  R  E  I  E  K  L  A    510
1531 GCCAGTTTATGGTTATGGAAGAGTGACATCGCTTCCCATTTTAGTAACAAAAGGAAGAAGTGTGTCCGTGATTGTGAAAAGTACAAGCCTGGCGTGTTG
     A  S  L  W  L  W  K  S  D  I  A  S  H  F  S  N  K  R  K  K  C  V  R  D  C  E  K  Y  K  P  G  V  L    543
1630 CTGGGGTTTAACATGAAAGAATTAAATAAAGTCAAGCATGAGATGGATTTTGATGCTGAGTGGCTATTTGAAAATCATGATGAGAAGGATTCCAGAGTC
     L  G  F  N  M  K  E  L  N  K  V  K  H  E  M  D  F  D  A  E  W  L  F  E  N  H  D  E  K  D  S  R  V    576
1729 AATGCTAGTAAGACTGCTGACAAAAAGCTCAACCTTGGGAAGGAAGATGACAGTTCCTCAGACAGTTTTGAAAATTTGGAAGAAGAATCCAATGAAAGT
     N  A  S  K  T  A  D  K  K  L  N  L  G  K  E  D  D  S  S  S  D  S  F  E  N  L  E  E  E  S  N  E  S    609
1828 GGTAGCCCTTTTGACCCTGTTTTTGAAGTTGAACCTAAAATCTCTAACGATAACCCAGAGGAACATGTACTGAAGGTAATTCCTGAGGATGCTTCAGAA
     G  S  P  F  D  P  V  F  E  V  E  P  K  I  S  N  D  N  P  E  E  H  V  L  K  V  I  P  E  D  A  S  E    642
```

FIG. 12A.

```
1927 TCTGAGGAGAAGCTAGACCAAAAAGAGGATGGTTCAAAATACGAAACTATTCATTTGACTGAGGAACCAACCAAACTAATGCACAATGCATCTGATAGT
      S  E  E  K  L  D  Q  K  E  D  G  S  K  Y  E  T  I  H  L  T  E  E  P  T  K  L  M  H  N  A  S  D  S   675
2026 GAGGTTGACCAAGACGATGTTGTTGAGTGGAAAGACGGTGCTTCTCCATCTGAGAGTGGGCCTGGATCCCAACAAGTGTCAGACTTTGAGGACAATACC
      E  V  D  Q  D  D  V  V  E  W  K  D  G  A  S  P  S  E  S  G  P  G  S  Q  Q  V  S  D  F  E  D  N  T   708
2125 TGCGAAATGAAACCAGGAACCTGGTCTGACGAGTCTTCCCAAAGCGAAGATGCAAGGAGCAGTAAGCCAGCTGCCAAAAAAAAAGGCTACCATGCAAGG
      C  E  M  K  P  G  T  W  S  D  E  S  S  Q  S  E  D  A  R  S  S  K  P  A  A  K  K  K  G  Y  H  A  R   741
2224 TGA
      *
```

Single underline - homologies to hsp60 of ADNP.
Double underline - Glycosilation sites.
Bold + Double underline -
1. Zinc finger C2h2 type, domains.
2. Glutaredoxin active site (amino acid no. 234-238)

Bold - potential proteolic cleavage site.

H3

FIG. 12B.

H7 clone

```
     AAAACCAGGACTATCGGACAAAACCTTTCTGCTGCAGCGCTTGTCCATTTTCCTCAAAATTCTTCTCTGCCTACAAAAGTCATTTCCGCAATGTCCAT

     AGTGAAGACTTTGAAAATAGGATTCTCCTTAATTGCCCCTACTGTACCTTCAATGCAGACAAAAAGACTTTGGAAACACACATTAAAATATTTCATGCT

     CCGAACGCCAGCGCACCAAGTAGCAGCTTCAGCACTTTCAAAGATAAAACCAAAAATGATGGCCTTAAACTTAAGCAGGCTGACAGTGTAGAGCAAGCT

     GTTTATTACTGTAAGAAGTGCACTTACCGAGATCCTCTTTATGAAATAGTTAGGAAGCACATTTACAGGGAACATTTTCAGCATGTGGCAGCACCTTAC

     ATAGCAAAGGCAGGAGAAAAATCACTCAATGGGGCAGTCCCCTTAGGCTCGAATGCCCGAGAAGAGAGTAGTATTCACTGCAAGCGATGCCTTTTCATG
                                                                                                      M
     CCAAAGTCCTATGAAGCTTTGGTACAGCATGTCATCGAAGACCATGAACGTATAGGCTATCAGGTCACTGCCATGATTGGGCACACAAATGTAGTGGTT
     P  K  S  Y  E  A  L  V  Q  H  V  I  E  D  H  E  R  I  G  Y  Q  V  T  A  M  I  G  H  T  N  V  V  V
54   CCCCGATCCAAACCCTTGATGCTAATTGCTCCCAAACCTCAAGACAAGAAGAGCATGGGACTCCCACCAAGGATCGGTTCCCTTGCTTCTGGAAATGTC
     P  R  S  K  P  L  M  L  I  A  P  K  P  Q  D  K  K  S  M  G  L  P  P  R  I  G  S  L  A  S  G  N  V    15
45   CGGTCTTTACCATCACAGCAGATGGTGAATCGACTCTCAATACCAAAGCCTAACTTAAATTCTACAGGAGTCAACATGATGTCCAGTGTTCATCTGCAG
     R  S  L  P  S  Q  Q  M  V  N  R  L  S  I  P  K  P  N  L  N  S  T  G  V  N  M  M  S  S  V  H  L  Q    48
144  CAGAACAACTATGGAGTCAAATCTGTAGGCCAGGGTTACAGTGTTGGTCAGTCAATGAGACTGGGTCTAGGTGGCAACGCACCAGTTTCCATTCCTCAA
     Q  N  N  Y  G  V  K  S  V  G  Q  G  Y  S  V  G  Q  S  M  R  L  G  L  G  G  N  A  P  V  S  I  P  Q    81
243  CAATCTCAGTCTGTAAAGCAGTTACTTCCAAGTGGAAACGGAAGGTCTTATGGGCTTGGGTCAGAGCAGAGGTCCCAGGCACCAGCAAGATACTCCCTG
     Q  S  Q  S  V  K  Q  L  L  P  S  G  N  G  R  S  Y  G  L  G  S  E  Q  R  S  Q  A  P  A  R  Y  S  L    114
342  CAGTCTGCTAATGCCTCTTCTCTCTCATCGGGCCAGTTAAAGTCTCCTTCCCTCTCTCAGTCACAGGCATCCAGAGTGTTAGGTCAGTCCAGTTCCAAA
     Q  S  A  N  A  S  S  L  S  S  G  Q  L  K  S  P  S  L  S  Q  S  Q  A  S  R  V  L  G  Q  S  S  S  K    147
441  CCTGCTGCAGCTGCCACAGGCCCTCCCCCAGGTAACACTTCCTCAACTCAAAAGTGGAAAATATGTACAATCTGTAATGAGCTTTTTCCTGAAAATGTC
     P  A  A  A  A  T  G  P  P  P  G  N  T  S  S  T  Q  K  W  K  I  C  T  I  C  N  E  L  F  P  E  N  V    180
540  TATAGTGTGCACTTCGAAAAAGAACATAAAGCTGAGAAAGTCCCAGCAGTAGCCAACTACATTATGAAAATACACAATTTTACTAGCAAATGCCTCTAC
     Y  S  V  H  F  E  K  E  H  K  A  E  K  V  P  A  V  A  N  Y  I  M  K  I  H  N  F  T  S  K  C  L  Y    213
639  TGTAATCGCTATTTACCCACAGATACTCTGCTCAACCATATGTTAATTCATGGTCTGTCTTGTCCATATTGCCGTTCAACTTTCAATGATGTGGAAAAG
     C  N  R  Y  L  P  T  D  T  L  L  N  H  M  L  I  H  G  L  S  C  P  Y  C  R  S  T  F  N  D  V  E  K    246
738  ATGGCCGCACACATGCGGATGGTTCACATTGATGAAGAGATGGGACCTAAAACAGATTCTACTTTGAGTTTTGATTTGACATTGCAGCAGGGTAGTCAC
     M  A  A  H  M  R  M  V  H  I  D  E  E  M  G  P  K  T  D  S  T  L  S  F  D  L  T  L  Q  Q  G  S  H    279
837  ACTAACATCCATCTCCTGGTAACTACATACAATCTGAGGGATGCCCCAGCTGAATCTGTTGCTTACCATGCCCAAAATAATCCTCCAGTTCCTCCAAAG
     T  N  I  H  L  L  V  T  T  Y  N  L  R  D  A  P  A  E  S  V  A  Y  H  A  Q  N  N  P  P  V  P  P  K    312
936  CCACAGCCAAAGGTTCAGGAAAAGGCAGATATCCCTGTAAAAAGTTCACCTCAAGCTGCAGTGCCCTATAAAAAAGATGTTGGGAAAACCCTTTGTCCT
     P  Q  P  K  V  Q  E  K  A  D  I  P  V  K  S  S  P  Q  A  A  V  P  Y  K  K  D  V  G  K  T  L  C  P    345
1035 CTTTGCTTTTCAATCCTAAAAGGACCCATATCTGATGCACTTGCACATCACTTACGAGAGAGGCACCAAGTTATTCAGACGGTTCATCCAGTTGAGAAA
     L  C  F  S  I  L  K  G  P  I  S  D  A  L  A  H  H  L  R  E  R  H  Q  V  I  Q  T  V  H  P  V  E  K    378
1134 AAGCTCACCTACAAATGTATCCATTGCCTTGGTGTGTATACCAGCAACATGACCGCCTCAACTATCACTCTGCATCTAGTTCACTGCAGGGGCGTTGGA
     K  L  T  Y  K  C  I  H  C  L  G  V  Y  T  S  N  M  T  A  S  T  I  T  L  H  L  V  H  C  R  G  V  G    411
1233 AAGACCCAAAATGGCCAGGATAAGACAAATGCACCCTCTCGGCTTAATCAGTCTCCAAGTCTGGCACCTGTGAAGCGCACTTACGAGCAAATGGAATTT
```

FIG. 13A.

```
     K  T  Q  N  G  Q  D  K  T  N  A  P  S  R  L  N  Q  S  P  S  L  A  P  V  K  R  T  Y  E  Q  M  E  F    444
1332 CCCTTACTGAAAAAACGAAAGTTAGATGATGATAGTGATTCACCCAGCTTCTTTGAAGAGAAGCCTGAAGAGCCTGTTGTTTTAGCTTTAGACCCCAAG
     P  L  L  K  K  R  K  L  D  D  D  S  D  S  P  S  F  F  E  E  K  P  E  E  P  V  V  L  A  L  D  P  K    477
1431 GGTCATGAAGATGATTCCTATGAAGCCAGGAAAAGCTTTCTAACAAAGTATTTCAACAAACAGCCCTATCCCACCAGGAGAGAAATTGAGAAGCTAGCA
     G  H  E  D  D  S  Y  E  A  R  K  S  F  L  T  K  Y  F  N  K  Q  P  Y  P  T  R  R  E  I  E  K  L  A    510
1530 GCCAGTTTATGGTTATGGAAGAGTGACATCGCTTCCCATTTTAGTAACAAAAGGAAGAAGTGTGTCCGTGATTGTGAAAAGTACAAGCCTGGCGTGTTG
     A  S  L  W  L  W  K  S  D  I  A  S  H  F  S  N  K  R  K  K  C  V  R  D  C  E  K  Y  K  P  G  V  L    543
1629 CTGGGGTTTAACATGAAAGAATTAAATAAAGTCAAGCATGAGATGGATTTTGATGCTGAGTGGCTATTTGAAAATCATGATGAGAAGGATTCCAGAGTC
     L  G  F  N  M  K  E  L  N  K  V  K  H  E  M  D  F  D  A  E  W  L  F  E  N  H  D  E  K  D  S  R  V    576
1728 AATGCTAGTAAGACTGCTGACAAAAAGCTCAACCTTGGGAAGGAAGATGACAGTTCCTCAGACAGTTTTGAAAATTTGGAAGAAGAATCCAATGAAAGT
     N  A  S  K  T  A  D  K  K  L  N  L  G  K  E  D  D  S  S  S  D  S  F  E  N  L  E  E  E  S  N  E  S    609
1827 GGTAGCCCTTTTGACCCTGTTTTTGAAGTTGAACCTAAAATCTCTAACGATAACCCAGAAGAACATGTACTGAAGGTAATTCCTGAGGATGCTTCAGAA
     G  S  P  F  D  P  V  F  E  V  E  P  K  I  S  N  D  N  P  E  E  H  V  L  K  V  I  P  E  D  A  S  E    642
1926 TCTGAGGAGAAGCTAGACCAAAAAGAAGATGGTTCAAAATACGAAACTATTCATTTGACTGAGGAACCAACCAAACTAATGCACAATGCATCTGATAGT
     S  E  E  K  L  D  Q  K  E  D  G  S  K  Y  E  T  I  H  L  T  E  E  P  T  K  L  M  H  N  A  S  D  S    675
2025 GAGGTTGACCAAGACGATGTTGTTGAGTGGAAAGACGGTGCTTCTCCATCTGAGAGTGGGCCTGGATCCCAACAAGTGTCAGACTTTGAGGACAATACC
     E  V  D  Q  D  D  V  V  E  W  K  D  G  A  S  P  S  E  S  G  P  G  S  Q  Q  V  S  D  F  E  D  N  T    708
2124 TGCGAAATGAAACCAGGAACCTGGTCTGACGAGTCTTCCCAAAGCGAAGATGCAAGGAGCAGTAAGCCAGCTGCCAAAAAAAAGGCTACCATGCAAGGT
     C  E  M  K  P  G  T  W  S  D  E  S  S  Q  S  E  D  A  R  S  S  K  P  A  A  K  K  K  A  T  M  Q  G    741
2223 GACAGAGAGCAGTTGAAATGGAAGAATAGTTCCTATGGAAAAGTTGAAGGGTTTTGGTCTAAGGACCAGTCACAGTGGAAGAATGCATCTGAGAATGAT
     D  R  E  Q  L  K  W  K  N  S  S  Y  G  K  V  E  G  F  W  S  K  D  Q  S  Q  W  K  N  A  S  E  N  D    774
2322 GAGCGCTTATCTAACCCCCAGATTGAGTGGCAGAATAGCACAATTGACAGTGAGGATGGGGAACAGTTTGACAACATGACTGATGGAGTAGCTGAGCCC
     E  R  L  S  N  P  Q  I  E  W  Q  N  S  T  I  D  S  E  D  G  E  Q  F  D  N  M  T  D  G  V  A  E  P    807
2421 ATGCATGGCAGCTTAGCCGGAGTTAAACTGAGCAGCCAACAGGCCTAAGTGCCAGGTTCCCTGGCATTGGTGACATGCTGCAGCCTGGAACTCTGATCT
     M  H  G  S  L  A  G  V  K  L  S  S  Q  Q  A*                                                        822
2520 CCAGTGTGACTGCAAAGCTGTCTTCTCACTGGTACTGCCTTGTGAGTACTGGTTGGACTGTGGGGCATGTGGCCGCTGCAGTTCCAGTGGTTATTTCTA

2619 AGTCTATGACAGGACAGGCTGTTCTTGCTTCAGAACCTTCTCTGACAGACACGGTAACTAAATGTGAAAAACCAATAAGCTGGTGACTCATGAATACAC

2718 ACGAGGAAAAGCAGAGGTTTATTTTATCTGCCTTTTCAACATTTCTTTCCCTCTGTGAAATGATTGGTCAGATGTCTTTGAGAAGTGTTAAACTAATTC

2817 ACATGGTAGTGTAGGGCCAACATACAAGCTACCAGTCTAATGTGTATAGTAGACTTTGGGAAAAGCGATTTTTTTTCATGTATTCATTCTGAATAGTTG

2916 AAATGTATATTTGTACAGTCTTTTAGACCTATTCAAGTGATGCTCATGATCCTGTTACTGTGTGCCCATCATAGATTTCTTTTTTAGTGTTGCCCTTG

3015 CTGTGTAATAAACGCTCTATCTAGTTTACCTAGCAAAAGCTCAAAACTGCGCTAGTATGGACTTTTTGGACAGACTTAGTTTTTGCACATAACCTTGTA

3114 CAATCTTGCAACAGAGGCCAGCCACGTAAGATATATATCTGGACTCTCTTGGATTATAGGATTTTTCTTGGTCTGAATATCCTTGACATTACAGCTGTC
```

FIG. 13B.

3213 AAAAACAAAAACTGGTATTTCAGATCTGTTTTCTGAAATCTTTTAAGCTAAAATCACATGCAAGAATTGACTTTGCAGCTACTAATTTTGACACCTTTT

3312 AGATCTGTATAAAAGTGTGTTGTGTTGAAGCAGCAAACCAATGAGTGCTGCATTTTGGATATTTAGTTTTATCTTTAGTTCAACACCATCATGGTGGAT

3411 TCATTTATACCATCTAATATATGACACACTGTTGTAGTATGTATAATTTTGTGATCTTTATTTTCCCTTTGTATTCATTTTAAGCATCTAAATAAATTG

3510 CTGTATTGTGCTTAATGTAAAAAAAAAAAAAAAAAAA

Bold: Putative initiator methionine
Bold underlined: initiator methionine in the mouse sequence (numbers of nucleic acids and amino acids is according to the mouse sequence).
Bold, italic, double underline: polymorphic site

FIG. 13C.

```
  1 AATTGTTGGG TGATGAGAAA GAGAGCTGTT TGCCTTCCGT GTTGGTCATC
 51 AAGGTCTGCG TGCATTGCAA CAGTGTCACC TGTGAGTTCC TGTGTCTGAA
101 GCCGAGAAGA TCCACAAAAT GAGGCTTTTC CATAGTTGGT TTGTGTTTTT
151 AACAAGAAAA TGGAGAGGCT TTTTGTTTGT TTTTGTTTTT GTTTTTTTGC
201 CTCTGACTTC TCTCTGAAAC CAGCCAACAA GTACAACTAG CAATTTTTAA
251 AGATTTAGCA AGAACTTGCA CTGAGTTTTC ATTTACAGGA GCACAAATAA
301 AAATATTTGA TTCAAAAATG CATCTGAGTT CTTTTAATTT TTCCTGCAGG
351 AGAAACCTCT AAAAGTCATT GCCTTGCAGA GTTTCTGGGA ATGCCTGGGG
401 GAGGAGCCTG GAACTTGTAA CTGCTTGCCT TGAGTGGCCT TCTCACTCTG
451 GTTTCTGTTC TGTTTTGTTT CGTTTGTTTT TT
```

FIG. 14.

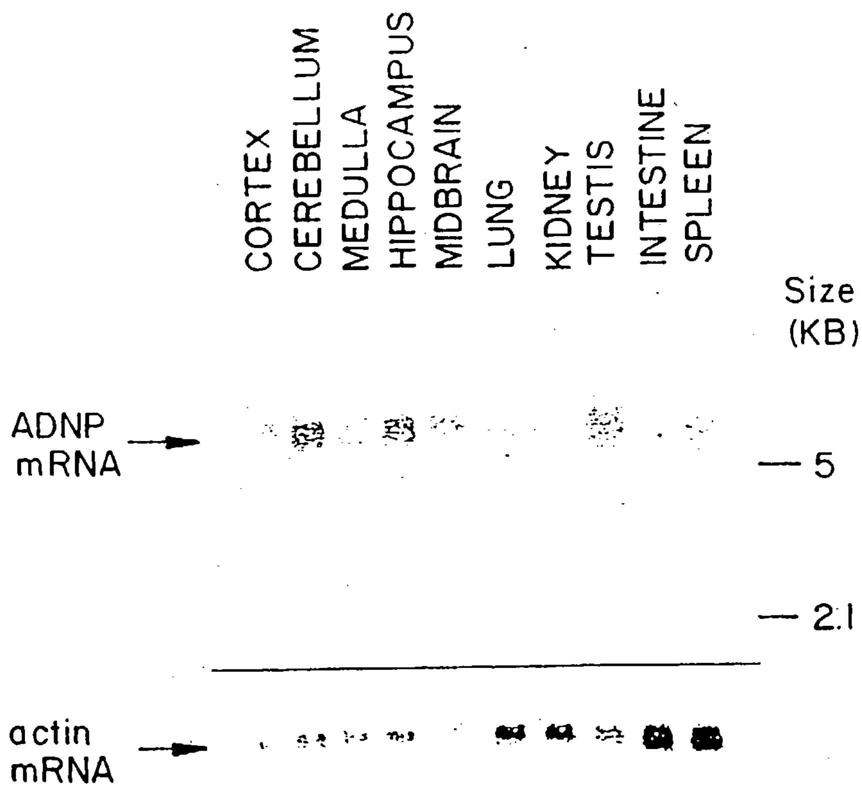

CORTEX
CEREBELLUM
MEDULLA
HIPPOCAMPUS
MIDBRAIN
LUNG
KIDNEY
TESTIS
INTESTINE
SPLEEN
Size (KB)
ADNP mRNA
— 5
— 2.1
actin mRNA

FIG. 15.

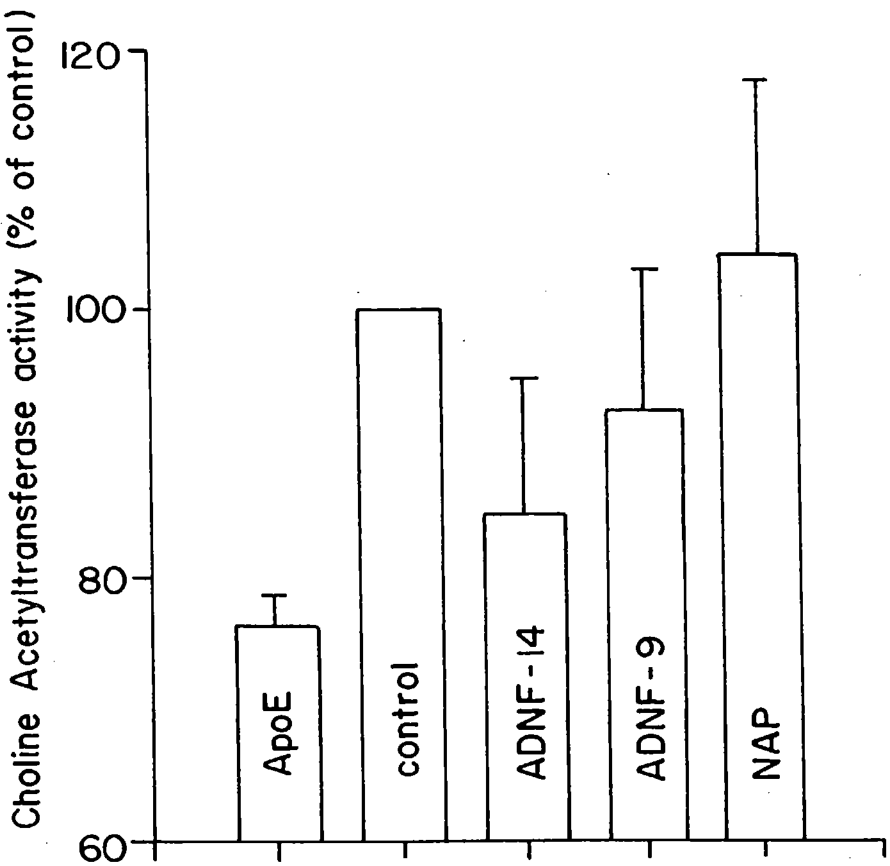

Choline Acetyltransferase activity (% of control)
120
100
80
60
ApoE
control
ADNF-14
ADNF-9
NAP

FIG. 16

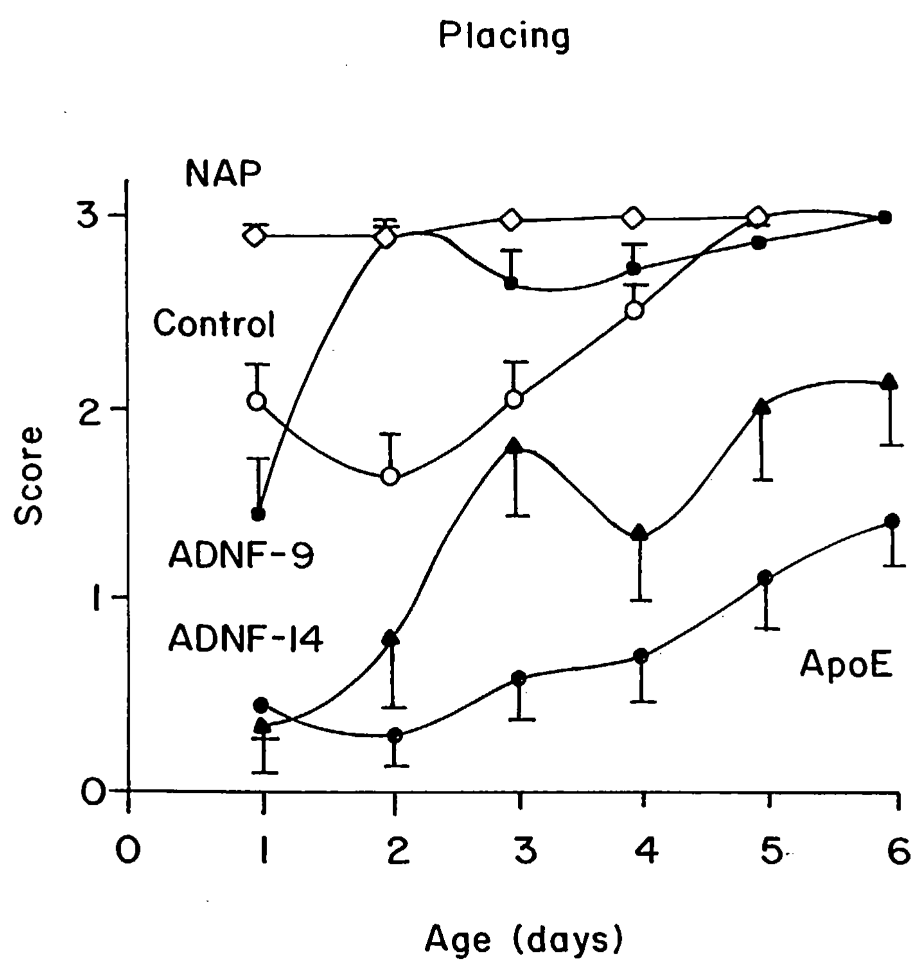

Placing
NAP
Control
ADNF-9
ADNF-14
ApoE
Score
0
1
2
3
0
1
2
3
4
5
6
Age (days)

FIG. 17

Polymorphism

H6	clone	GAGTTAAACT	GAGCAGCCAA	CAGGCCTAAG	TGCCAGGTTC	CCTGGCATTG
H10	clone	GAGTTAAACT	GANCANCCAN	CAGGCCTAAG	TGCCAGGTTN	CCTGGCGTTG
H3	clone	GAGTTAAACT	GAGCAGCCAA	CAGGCCTAAG	TGCCAGGTTC	CCTGGCGTTG
H12	clone	GAGTTAAACT	GAGCAGCCAA	CAGGCCTAAG	TGCCAGGTTC	CCTGGCGTTG
H7	clone	GAGTTAAACT	GAGCAGCCAA	CAGGCCTAAG	TGCCAGGTTC	CCTGGCATTG
H4	clone	GAGTTAAACT	GAGCAGCCAA	CAGGCCTAAG	TGCCAGGTTC	CCTGGCGTTG
H2	clone	GAGTTAAACT	GAGCAGCCAA	CAGGCCTAAG	TGCCAGGTTC	CCTGGCATTG

Polymorphic site: A → G transition

FIG. 18.